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FIG. 1

Sequence	MB DNA (%)	EC DNA (%)	fold (MB/EC)	GC0GC0=	0.2336	0.0654	3,58
		()	(,,	GCCGTC=	0.1008	0.0296	3.41
GGCGCC=	0.1462	0.0020	73.12	GGCGGC=	0.2237	0.0662	3.38
GCCGGC=	0.2317	0.0062	37.19	GCCGGT=	0.1302	0.0402	3.24
GTCGAC=	0.0990	0.0116	8.56	CCCGGC=	0.1183	0.0365	3.24
CTCGAG=	0.0299	0.0038	7.96	GACGGC=	0.1033	0.0327	3.16
CCCGGG=	0.0645	0.0091	7.13	CCCGCG=	0.0824	0.0263	3.13
CACGTG=	0.0205	0.0030	6.74	GCCGGG=	0.1165	0.0373	3.13
CCCGAG=	0.0451	0.0069	6.58	CGCGGG=	0.0849	0.0273	3.11
CTCGGG=	0.0392	0.0068	5.75	ACCGGC=	0.1242	0.0405	3.07
GCCGAC=	0.1435	0.0297	4.83	GGCGGG=	0.0382	0.0323	3.04
GTCGGC=	0.1400	0.0295	4.74	000600=	0.0995	0.0329	3.02
CTCGGC=	0.1021	0.0217	4.71	OGCGGT=	0.1117	0.0372	3.00
GCCGAG=	0.1000	0.0218	4.58	ACCGCG=	0.1090	0.0368	2.97
GACGAG=	0.0493	0.0120	4.10	ACCGAG=	0.0511	0.0175	2.92
GCCGCG=	0.1781	0.0435	4.09	GTCGGA=	0.0331	0.0118	2.80
GACGTC=	0.0619	0.0151	4.09	GGCGAC=	0.1005	0.0360	2.80
GTCGAG=	0.0677	0.0166	4.08	CTCGGT=	0.0494	0.0178	2.78
GTCGTC=	0.0755	0.0192	3.93	GTCGCC=	0.1056	0.0383	2.76
CTCGAC=	0.0643	0.0165	3.90	GTCGCG=	0.0884	0.0323	2.74
CCCGAC=	0.0676	0.0175	3.86	CACGTC=	0.0430	0.0158	2.73
CT CGT C=	0.0501	0.0130	3.86	TCCGAC=	0.0326	0.0121	2.70
CGCGGC=	0.1751	0.0455	3.85	CGCGAC=	0.0852	0.0320	266
GTCGGG=	0.0627	0.0165	3.79				
TCCGAG=	0.0203	0.0054	3.78				
GACGAC=	0.0747	0.0199	3.76	Average	0.0498	0.0288	
CTCGGA=	0.0202	0.0054	3.73	Sum	12.7440	7.3665	

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FIG. 2

	SEQ	UENCE	ID No.:	-	SEQ	UENCE I	D
M	B-ODN 4/5 (-CGXXCG)	XXCG-) 16	MB-	-ODN 5/5 (-CGXXXCG)	(XXCG-)	
No.	Sequence	Score		No.	Sequence	Score	
. 1	CTCCAcqGGcqGCAcqGCCA	11811	17	1	TGCTeqTGGeqGCTeqGCAG	12868	ľ
2	TGTCTcqGGcqGCAcqGTTG	11773	18	2	GAGGeoGCTeoGTGeoGGTC	12599	1
3	CAAGGeqGTeqGCTeqATGG	11538	19	3	TTGGcqGCAcqCAAcqCCTC	11345	1
4	AACTG coGAc oTGG coGCAG	10931	20	4	GAAGcaTTGcaGGGcaGCCC	11280	١.
5	GTCAGeqGAeqTGGeqGCTC	10829	21	5	AAGGcqTGGcqGCTcqTGGA	11258	
6	AAAG GegTGegGGTegGCCC	10697	22	6	CAGGegATGegCCTegGCTC	10614	l.
1	CTCAGegGGegGCAegTGCA	10670	23	7	GTTGcqGGAcqAGTcqGCAT	10297	ľ
ī	CACAAcqGGcqCCTcqGCTT	10319	24	8	GGGGcqGGTcqACTcqACCA	10243	ŀ
9	ATGARegGGegGCTegAGCC	10240	25	9	TGGTe qGGGe qGGTeqACTC	10153	l i
10	GATGGegATegGCAegCCCA	10199	26	10	ATCA cqCTAcqGGGcqGCCA	10063	
11	CAGCAcqTGcqTGGcqGCAT	9962	27	11	GTGGcqCCAcqAGTcqACAT	10059	1
12	GC TGGcqGGcqAGGcqATTC	9855	28	12	AAGG c qGC Tc qCATcqATGG	10036	1
13	TGTTGcqCTcqGCTcqGCAG	9839	29	13	GRGGe qG GGe qGGT eqRTCT	9743	1
14	GGTGGcqGTcqAGGcqCTCT	9728	30	14	AATTeqTGGeqGCTeqTGCA	9712	į
15	GGTGGeqCAcqCCTeqGCCC	9259	31	15	CAGG c qGTGc qGTG cqGCAT	9657	1
16	GGGGGeqGTeqCCTeqCTAA	9250	32	16	TAGGeqCTTeqAGTeqGCAC	9655	è
17	GACA TegGTegGCA egTCAG	9098	33	17	GTGAcgTCAcgGGTcgGCAG	9390	6
15	CCAG TegGGegGGGggCTGG	9022	34	13	GCTTcgAGTcgGCAcgCCAG	9269	6
19	TC TGGcqGTcqAAGcqGCCC	8953	35	19	GTGTeqGGGeqAGGeqACCA	9164	6
20	CAACTeqATeqGGGeqCCCA	8878	36	20	TTGGcgTTGcgTGTcgGCCT	9034	6
21	TTTGGcqGTcqGTGcqCAGC	8869	37	21	TCATe gATGe gGG GegCCAC	8959	6
22	CCAGGeqGTeqGTGeqCAGG	8869	38	22	GAGGcqGGGcqGGGGqGAGA	8873	6
23	CTCCTeqGTeqAGGeqGTGG	8844	39	23	TAGG coATGcgCAGcgCCTG	8845	6
24	ACCATeqGGeqCCAegTCTC	8780	40	24	CAGGogGTGogGCAcgCAGT	8703	6
25	CAACAcgATcgTGTcgGCTG	8615	41	25	CTGAegCCTegGCTegAGCT	8642	7

393	GTGTTeqAAeqCTAeqAACC	1681	42	352	ATTRe qC TGe qAAA eq CAGT	1807	7
394	ARGTRegARegATGegAGAA	1637	43	353	TARTe qGARe q TAR eqATCC	1713	7.
395	ACTA Gog TÃo g CÃG og ÃÃT C	1539	44	354	CATGogTAAogTTAogGAAA	1219	7

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FIG. 3

a)

SEQUENCE ID No.:

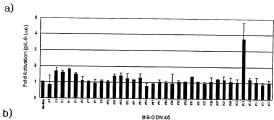
MB-ODN 4/5 (-CGXXCGXXXCG-) 74

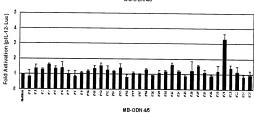
MB-ODN 5/5 (-CGXXXCGXXXCG-)

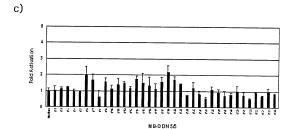
		1
O DN	Sequence	7]
MB-0DN4/5-1	CCAGTCGGGCGGGGGGCGCTGG	7 75
MB-0DN4/5-2	GCTGGCGGGGCGAGGGGATTC	1176
MB-0DN4/5-8	ACCAGCGGGCGAGTCGCCTG	1177
MB-0DN4/5-4	GGTGGGGGGGTTGCGGATC	1 78
MB-0DN4/5-5	GGCAGCGGGGCGCATCGCCAG	1179
MB-0DN4/5-8	CTTGGCGGGGGGCGCGACCA	1180
MB-00N4/5-7	AACTGCGGACGTGGCGGCAG	1 81
MB-0DN4/5-8	GGTCACGGTCGGATCGATTC	1 82
MB-00N4/5-9	FFFGGCGGTGCGCAGC	1183
MB-0DN4/5-10	CG T CGCC GT CGA GG CGC TC T	1 84
MB-0DN4/5-11	GGTGGCGGTCGAGGCGCTCT	1185
MB-0DN4/5-12	TTTGTCGGTCGCAACGAAAA	1186
MB-ODN4/5-18	CATGTCGAGCGGATCGGCAC	1 87
MB-0DN4/5-14		1 88
MB-0DN4/5-15	Pregregageereregeere	1 89
MB-0DN4/5-16	AGCATCGAGCGCAGCGTGGT	1 90
MB-0DN4/5-17	GG CA GCGAG CGCAA CGA CAC	91
MB-0DN4/5-18	CTCATCGAGCGCCACGGCAG	92
MB-00N4/5-19	AFGCTCGAGCGCCTCGGCCC	93
MB-0DN4/5-20	GCCTTCGAACGGGTCGAGGG	94
MB-00N4/5-21	eatecegaaceteaceteat	95
MB-0DN4/5-22	CTTGTCGAACGTCTCGGCCA	96
ИB-ODN4/5-28	CACATCGAACGCTTCGACAC	97
MB-0DN4/5-24	CAGTTCGATCGAGACGACCC	98
MB-0DN4/5-25	CTACCCCATCCATCCCCCAA	99
ИВ-ODN4/5-28	CAACACGATCGTGTGGGGTG	100
ИВ-ODN4/5-27	CTAGGCGATCGCAACGAAGT	101
AB-0DN4/5-29	CCACACGATCGCCACGGTGG	102
/IB-ODN4/5-29	GCCAGCGTGCGTGACGACTT	103
/IB-ODN4/5-30	TAAGGCGTGCGCATCGATAT	104
/IB-ODN4/5-81	ACCACCOTTC CTCTCCCCCT	105
AB-ODN4/5-82	refreedexederedected	106
/IB-ODN4/5-88	CTGGGCGCACGCACGCTGG	107
/IB-ODN4/5-74	GGCA GCGCAC GCA GCGCAAC	108
AD_ODMA (E.Z.E.)	GCAGGCGCTCGTCACGCCCC	1

			l	
Į	O DN	Sequence	7	
Į	MB-ODN5/5-1	CATGCCCATCCCTCCCCTCC		111
İ	MB-ODN5/5-2	CAGGCGGTGCGCAACGCCTG	1 1	112
ı	MB-ODN5/5-8	CATCCCCTCCCCATCCCCAA	1 1	113
I	MB-ODN 5/5-4	GAGGCGGTGCGCCACGTGCT	1 1	114
	MB-ODN5/5-5	CCACCCCCCCCACACCACAA		115
١	MB-ODN5/5-8	Pegrega ggc gr rgcg gga c		116
l	MB-ODN5/5-7	A CAGOGA G FO GO FG CG CCA C		117
Ì	MB-ODN5/5-8	Paggegaagegatgeggee		118
l	MB-ODN5/5-9	PCAGCGAAGCGGTGCGCCCA		119
l	MB-0DN5/5-10	A T C T C GA A GC GC T G C G A G G G	1 1	120
ı	MB-00N\$/5-11	GGGTCGAATCGTGTCGCCTC	1 1	21
ŀ	MB-ODNS/5-12	PAGGCGATGCGCAGCGCCTG		22
l	MB-ODNS/5-18	A TOGGO CAT GO GO TOGGO CTG		23
	MB-ODN5/5-14	GGGTCGACACGCTGCGATTG		24
	M B-ODN 5/5-15	recrearesesseressels	1	25
	MB-ODNE/5-18	C CAGCGTGGCGA TGCGGGCA	1	26
	MB-ODN5/5-17	G CATCOT GGC GCAG CG CATG	l li	27
	MB-ODN5/5-18	rggac grercgrag cg cagg	1	28
	MB-ODN 5/5-19	CTGGCGTAGCGCCTCGGCCT	1	29
	MB-ODN5/5-20	rrecerrecererecer	1	30
	MB-ODNS/5-21	AAATC CTT CC CCCACC CCAT	1	31
	M B-ODN5/5-22	ATCACGTTCCCCACCCCCTC	1	32
	M B-ODN 5/5-28	AAA TOGTOTOGAGGGGTTCC	1	33
	MB-00N5/5-24	G TG GC GCA GC GT GG CG GT GG	1	34
	M B-ODN 5/ 5-25	T GG GC GCA GC GG CACG CTAT	1	35
	MB-ODNS/5-28	PCTCCCCACCCCATCGTTCA	H	36
	M B-ODNS/ 5-27	PCGCCCCACCCTTACCAACT	l I	37
	M B-ODN5/5-28	GCCTCGCAGCGACACGTTGG	1	38
	M B-ODN 5/5-29	PPGGCGCAACGCAPCGGAGA	1	39
	MB-0DN5/5-80	G CA GC GC A AC GT TG CG CA T C	h	40
	MB-ODN 5/5-81	A CAAC GCA TC GCAT CGAG GA	- 1	41
	MB-ODNS/5-82	A GCAC GCTGC GGGTCGTCAG	1	42
	M B-ODN5/5-88	A CT GC GCT GC GG CA CGA CCC	1	43
	MB-00N5/5-84	GTCTCGCTGCGCAGCGGGGT	- 1	44
	MB-0DN5/5-85	CCCACCCTCCCTCACCTCCT	1	45
	MB-ODN 5/5-88	CTGACGCCTCGGCTCGAGCT	11.	46
			-	

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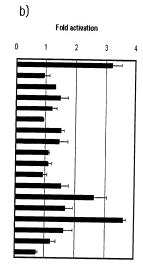


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FIG. 5

a)

SEQUENCE ID No :: ODN Sequence MB 4/5 #31 AGCAGCGTTCGTGTCGGCCT 147 #31.1 CAGCTCGTTCGTGTCGTGCT 148 #31.2 TGTGGCGTTCGTGTCGGTCT 149 #31.3 TGCAACGTTCGTGTCGCCAC 150 #31,4 GCCCCCGTTCGTGTCGGTAG 151 #31.5 GARCACGTTCGTGTCGGAAC 152 #31.6 CAGCACGTTCGTGTCGGACA 153 #31.7 TATGTCGTTCGTGTCGTCTT 154 #31.8 AAGGCCGTTCGTGTCGCTTG 155 #319 ATTTGCGTTCGTGTCGATTC 156 #31.10 GCTGCCGTTCGTCTCTCTT 157 #31.11 ATGGGCGTTCGTGTCGATCC 158 #31.12 CTATTCGTTCGTGTCCT 159 #31.13 GGGARCGTTCGTGTCGCTGC 160 #31.14 TGACTCGTTCGTGTCGCATG 161 #31.15 GTCATCGTTCGTGTCGAGAC 162 #31.16 TTGCACGTTCGTGTCGATGA 163 #31.17 CAGCACGITCGTGTCGGTCA 164



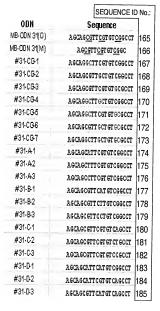
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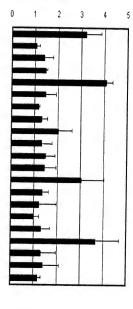
FIG. 6

a)

b)

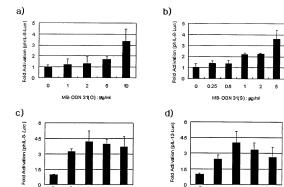
Fold Activation (phlL-8-Luc)





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FIG. 7



0

Medium

#31(0)

#31(S)

31.14(0) #31.14(S)

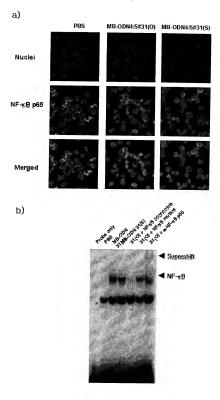
1.5 0

Medium #31(0) #31(S)

31.14(0) #31.14(S)

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FIG. 8



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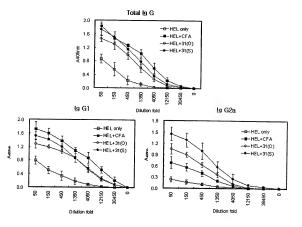


FIG. 10



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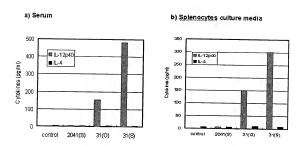
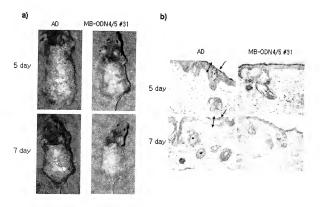


FIG. 12



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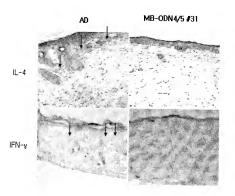
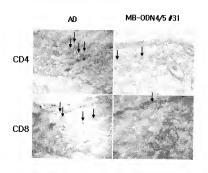


FIG. 14



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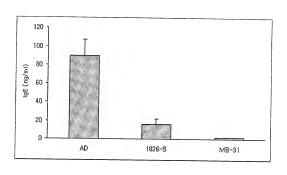


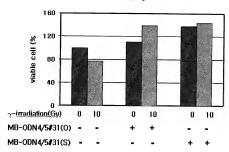
FIG. 16

MB-00N4/5#31 (10 µg/m)
0 2.5 5 10 h

Bcl-xS/L.→

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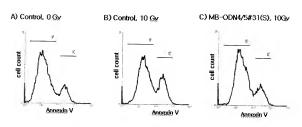


Fig.	γ -irradiation	MB-ODN 4/5 #31(S)	Marker	%Total
Α	0 Gy	(-)	M1 M2	73, 54 16, 709
В	10 Gy	(-)	M1 M2	58,82 27,24
С	10 Gy	(+)	M1 M2	65, 25 18, 71

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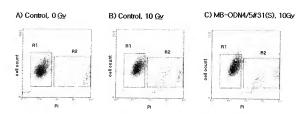


Fig.	γ - irradiation	MB-ODN 4/5 #31(s)	Region	%Total
Α	0 Gy	(-)	R1 R2	73, 30 16, 32
В	10 Gy	(-)	R1 R2	58, 93 25, 33
С	10 Gy	(+)	R1 R2	62, 82 20, 92